

OM of: US-09-805-550-4 to: EST:\* out\_format : pfs  
Date: Aug 31, 2002 6:39 AM

About: Results were produced by the Gencore software, version 4.5,  
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## Command line parameters:

-MODEL=frame+g2n.model -DEV=x1h  
-O=cgnt2.1/USP70\_spool/US09805550/runat\_29082002.160818.264/app\_query\_fasta-1-897  
-DB=EST -QFMT=fastap -SUFFIX=oligop2n.rst -GAPOP=4.500  
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPTOL=0.000 -LOOPEXT=0.000  
-CGAPOP=4.500 -CGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000  
-FGAPOP=6.000 -FGAPEXT=7.000 -TGAPOP=60.000 -TGAPEXT=60.000  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo  
-TRANS=human4.0.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=quality  
-THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NOR=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09805550 -CGCN1.1.3201 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLIPX -WAIT -THREADS=1

## Search information block:

Query: US-09-805-550-4

Query length: 368

Database: EST:\*

Database sequences: 13736207

Database length: -1841457050

Search time (sec): 2401.010000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000  
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

## score\_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Document
gb_est2:BE510592	+	135.00	2270.72	3.1e-117	407	BE510592 946054A04.y1 946 - tas
gb_est2:BE510591	-	121.00	2024.65	4.4e-104	365	BE510591 946054A04.x1 946 - tas
gb_est2:AI901927	-	101.00	1693.92	4.2e-85	479	AI901927 618012E05.x1 618 - int
gb_est2:BE655703	+	59.00	966.45	1.1e-45	315	BE655703 FM1.47.H02.b1.A008 FIC
gb_est2:BE650335	-	59.00	981.12	1.1e-45	605	BE650335 DGI.64.F06.b1.A002 dat
gb_est2:AI612200	-	58.00	968.12	1.1e-44	374	AI612200 486083C02.x1 486 - int
gb_est2:AM171897	+	56.00	930.37	1.4e-42	603	AM171897 618053E05.x1 618 - int
gb_est2:AM661449	+	41.00	664.17	6.8e-29	220	AM661449 ZEST000631 Maize Leaf,
gb_est2:AI948181	-	33.00	644.84	1.1e-26	460	AI948181 603037D08.x1 603 - str
gb_gss:BH257042	+	37.00	610.94	8.8e-25	463	BH257042 LDH5BAM000309F Zea me
gb_est2:BE471046	+	28.00	459.92	2.4e-16	409	BE471046 WHE0954.E12.J24Z whea
gb_est2:BE498178	+	28.00	459.17	2.5e-16	432	BE498178 WHE0954.E12.J24Z whea
gb_est2:BE517807	+	28.00	458.87	2.6e-16	448	BE517807 WHE0903.E10.J19ZS whea
gb_est2:BE629728	+	28.00	454.95	4.3e-16	725	BE629728 CC-est1CDEL29M6a1 TOM
gb_est2:AL370990	-	24.00	331.74	1.4e-12	315	AL370990 MB441B12F1 M6a1 TOM
gb_est2:AM684155	+	22.00	359.69	8.7e-11	374	AM684155 NE01B09NR1P1000 Nodul
gb_est2:BE517055	+	22.00	358.79	9.7e-11	398	BE517055 NXSL.008.F06.F NXSL (N
gb_est2:BM172975	+	22.00	357.73	1.1e-10	426	BM172975 900329 AVicentia marit
gb_est2:AI855539	+	22.00	356.39	1.1e-10	502	AI855539 sc20e06.y1 Gm-cl013 GI
gb_est2:AM562573	+	22.00	355.43	1.1e-10	565	AM562573 660066E09.y1 660 - Mix
gb_est2:AI725446	+	22.00	354.94	1.6e-10	600	AI725446 BMTG112207 Six-day CC
gb_est2:BE519032	+	22.00	354.94	1.6e-10	600	BE519032 EST46492 DSI1 Medicag
gb_est2:AM508593	+	22.00	353.81	1.8e-10	689	AM508593 s134e09.y1 Gm-cl1030 GI
gb_est2:AM053842	+	22.00	353.41	1.9e-10	723	AM053842 L30-225973 Ice plant I
gb_est2:BF268384	+	22.00	353.29	2.0e-10	734	BF268384 GA_EB0001K11f Gossyp
gb_est2:BG581659	+	22.00	352.86	2.1e-10	774	BG581659 EST453394 GVN Medicag
gb_est2:BG645488	+	22.00	352.51	2.2e-10	808	BG645488 EST507107 RV3 Medicag
gb_est2:BG585286	+	22.00	352.42	2.2e-10	817	BG585286 EST487049 GVM Medicag
gb_est2:BG585286	+	22.00	352.39	2.2e-10	820	BG585286 EST484135 GVM Medicag
gb_est2:BG445485	+	22.00	351.81	2.4e-10	880	BG445485 GA_EA0028M06f Gossyp
gb_est2:AV536745	+	21.00	340.18	1.0e-09	441	AV536745 Arabidopsis t
gb_est2:BE360629	+	21.00	339.42	1.1e-09	460	BE360629 DGI.64.F06.g1.A002 dat
gb_est2:BG368695	+	21.00	338.65	1.2e-09	503	BG368695 AVS22118 Arabidopsis t
gb_est2:AV522118	-	21.00	339.43	1.3e-09	556	AV522118 AVS22118 Arabidopsis t
gb_est2:BM360022	-	21.00	337.63	1.5e-09	629	BM360022 GA_EA0026M08r Gossyp
gb_gss:BH442147	-	21.00	335.95	1.8e-09	771	BH442147 BHM822F BOHN Brasili
gb_est2:BG445328	+	21.00	335.36	1.9e-09	810	BG445328 GA_EA0027L122f Gossyp

gb\_est2:BG445098 + 21.00 334.71 2.1e-09 899 | BG445098 GA\_EA0026M08f Goss  
gb\_est2:BM085190 + 20.00 321.82 1.1e-08 548 | BM085190 sc33303.y1 Gm-cl106  
gb\_est2:BF067283 + 20.00 320.74 1.3e-08 626 | BF067283 sc37908.y1 Gm-cl1067  
gb\_est2:BF724240 + 20.00 318.49 1.7e-08 825 | BF724240 GA\_EB0014N15f Goss  
gb\_est2:BG582388 + 20.00 318.20 1.8e-08 854 | BG582388 EST484131 GVN Medic  
gb\_est2:AM054457 - 19.00 313.16 3.4e-08 199 | AM054457 660007C12.x1 660 -  
gb\_est2:AV912395 - 19.00 303.97 1.1e-07 614 | AV912395 AV912395 K. Sato un

seq\_name: gb\_est2:BE510592

seq\_documentation\_block:

LOCUS BE510592 407 bp mRNA linear EST 07-AUG-2000

DEFINITION 946054A04.y1 946 - tassal primordium prepared by Schmidt lab Zea

maize cDNA, mRNA sequence.

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61  L u a s n l y s V a l a s n g l u a s p g l y p h e l e u a l a l m e t l e u s e r l y s g l y 77
|||||
102 A G A A T A A A C T C A T A G A T G G T T C T A G T T C A T G C T A G T A A G G G T 151
78  L y s T h r S e r G l y S e r T h r G l y T h r S e r S e r G l n H i s S e r a s n t h r P r 94
|||||
152 A A A A C A T C T G G T T C A C T G A A C T C A T C T C C A C A C C T C A A A C A C T C C 201
94  o A l a T h r A r g I n a l a P r o P r o l e u g l u a l a P r o g l n g l n a l a P r o g l n P 111
|||||
202 T G C A C A A G C A G G C A C C T C C T C T A G A G C C C C A C A C A A G C C T C A A C 251
111 r o P r o V a l a l a P r o l i e t h r T h r S e r G l n P r o g l u g l y l e u P r o a l a g l n 127
|||||
252 C C C C G G T G C A C C A A T T A C A C T T C A C C T G A G A G A C T T C C T G C A C A G 301
128 A l a P r o A s n T h r H i s A s p a s n A l a S e r A s n l e u S e r G l y A r g a s 144
|||||
302 G C A C C T A A C A C A T G A C A A T G C G G C A T C A A A T C T T C T G T G A A G G A A 351
144 n V a l a s p T h r l l e l e a s n g l n l e u m e t g l u m e t g l y g l y S e r T r P A 161
|||||
352 T G T T G A C A C A A T A T T A A C C A G C T A T G A G A T G G T G G G G A A G T T G G G 401
161 s p l y s 162
|||||
402 A C A A A 406

seq_name: gb_est2:BE510591
seq_documentation_block:
LOCUS BE510591 365 bp mRNA linear EST 07-AUG-2000
DEFINITION 946054A04.x1 946 - tassal primordium prepared by schmidt lab Zea
mays CDNA, mRNA sequence.
ACCESSION BE510591
VERSION BE510591.1 GI:9731839
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 365)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946054 row: A column: 04.
FEATURES
Source location/Qualifiers
1..365 /organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassal primordium prepared by Schmidt
lab"
/issue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="X10LR"
/note="Organ: tassels; Vector: HybriZAP, Site_1: EcorI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."
BASE COUNT 94 a 99 c 77 g 95 t
ORIGIN

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alignment_scores:
Quality: 121.00 Length: 121
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-4 x BE510591/rev ..
Align seg 1/1 to reverse of: BE510591 from: 1 to: 365

223 P r o l e u a s p l e u n p h e p r o g l n g l y a l a S e r a s n a l e g l y g l y a l a g l 239
|||||
363 C C A C T A G A A T C T T T C C C G A G G G G C C T C C A A T G C T G A G A G T G T G C T G G 314
239 y g l y g l y P r o l e u a s p h e l e u a r g a s n a s n p r o g l n p h e g l n a l a V a l a 256
|||||
313 T G S T G A C C A C T T G A T T T C T T A G A A A C A A T C C A G A G T T T C A A G C A G T T C 264
256 r g l u m e t V a l H i s T h r A s n P r o g l n l l e u g l n P r o m e t l e u V a l g l u 272
|||||
263 G G G A A A T G G T C C A T A C A A A T T T T G C A G C C T A T G C T G T T G A G 214
273 L e u S e r l y s G l n A s n P r o g l n l l e u a r g l e u l l e g l u g l u a s H i s a s 289
|||||
213 T T G A G C A A G C A G A A T C C T C A A A T T A G A G T T A G A G A G A A T C A T G A 164
289 p g l u p h e l e u g l n l e u l e u a s n g l u p r o p h e g l u g l y g l y g l u g l y A s p 306
|||||
163 T G A G T T C T T C A G T T A C T A A T A T A G C C T T T G A A G C G G G A G A G G G A A T T 114
306 h e l e u a s p g l n P r o g l u g l u a s p g l u m e t P r o H i s a l a l e S e r V a l t h r 322
|||||
113 T C T T A G C C A C C A C T G A G A G A T G A A A T G C T C A C G C A T A G T A G T T A C A 64
323 P r o g l u g l u g l n g l u a l a l l e g l y a r g l e u g l u S e r m e t g l y P h e a s p a r 339
|||||
63 C C A G A G A G A G C A G A G G C C A T T G A C G C T T G A C T C A T G C A T G G G T T C A C A G 14
339 g A l a r g V a l l l e 343
|||||
13 A C C A C C G C T T A T C 1

seq_name: gb_est1:A1901927
seq_documentation_block:
LOCUS A1901927 479 bp mRNA linear EST 27-JUL-1999
DEFINITION 618012E05.x1 618 - Inbred Tassal cDNA Library Zea mays CDNA, mRNA
sequence.
ACCESSION A1901927
VERSION A1901927.1 GI:5608260
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 479)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 618012 row: E column: 05.
FEATURES
Source location/Qualifiers
1..479

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/organism="Zea mays"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_lib="618 - Inbred Tassel cDNA library"
/tissue_type="tassel"
/dev_stage="tassel length from 0.1 to 2.5 cm"
/lab_host="XLOLR"
/note="Organ: tassel; Vector: pAD-GAL4-2.1 (Hybridap);
Inbred tassel library from Schmidt lab"
BASE COUNT      139 a      126 c      97 g      117 t
ORIGIN

alignment_scores:
  Quality: 101.00      Length: 101
  Ratio: 1.000      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-805-550-4 x AI901927/rev ..

Align seg 1/1 to reverse of: AI901927 from: 1 to: 479

268 PrometleuValGluLeuSerLySGlnAsnProGlnIleLeuArgLeuI 284
|||||
478 CCTATGCTGTTGAGTTCAGTTCCTGAGTTCCTGAGTTCCTGAGTTC 429
|||||
284 eglGluAsnHisAspGluPheLeuGlnLeuLeuAsnGluProPheGlu 301
|||||
428 TGAGGAGAAATCATGATGATGATTTCTTCAGTTCCTGAGTTCCTGAG 379
|||||
301 LylGluGluGlyAspPheLeuAspGlnProGluGluAsnGluMetProHis 317
|||||
378 GCGGAGAGGGGCGATTTCTTAGACCACTGAGAGGATGAATGCTCCAC 329
|||||
318 AlAlIleSerValThrProGluGluGlnGluAlaIleGlyArgLeuGlu 334
|||||
328 GCGATTAAGTTTACCCAGAGAGAGAGAGGCGCTTGAGCGCTTGAGTC 279
|||||
334 rmetGlyPheAspParGAlaArgValIleGluAlaPheLeuAlaCysAsp 351
|||||
278 CATGGGGTTGACAGACAGACGCGTTATCGAAGCATTTCTTAGCCGCGATA 229
|||||
351 rGAsnGluGluLeuAlaAlaAsnTyrLeuLeuGluHisAlaGlyGluGlu 367
|||||
228 GGAACGAGGAGTAGCAGCAAACTATCTCTTGAGCATGCTGCGAGGAA 179
|||||
368 Asp 368
178 GAT 176

seq_name: gb_est2:BF655703

seq_documentation_block:
LOCUS      BF655703      315 bp      mRNA      linear      EST 20-DEC-2000
DEFINITION F01_47_H02_b1_A003 Floral-Induced Meristem 1 (F01) Sorghum
propinquum cDNA, mRNA sequence.
ACCESSION  BF655703
VERSION     BF655703.1 GI:11920835
KEYWORDS   EST.
SOURCE     Sorghum propinquum.
ORGANISM   Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 315)
Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt
,L.H.
An EST database from Sorghum: floral-induced meristems
Unpublished (2000)
JOURNAL
COMMENT    Contact: Cordonnier-Pratt MM
            Department of Botany
            The University of Georgia

```

```

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmp@prattuga.edu
Sequences have been trimmed to exclude polyA, vector and regions
below paired quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence start: 54
High quality sequence stop: 217
POLYA=No.

FEATURES
    source
        1..315
            /organism="Sorghum propinquum"
            /db_xref="taxon:132711"
            /clone_lib="Floral-Induced Meristem 1 (F01)"
            /note="Organ: Floral-Induced meristems; Vector:
            pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
            EcoRI; mature plants were placed in a growth chamber for
            15 days with 16 hr darkness and 8 hr light (flowering is
            induced by short-day conditions); 16 days after being
            returned to the greenhouse under natural long days during
            late April/early May, meristems were harvested The
            library was made from poly-A RNA in the cloning vector
            lambda Zap II. Clones to be sequenced were prepared by
            mass excision."
BASE COUNT      82 a      96 c      91 g      46 t
ORIGIN

alignment_scores:
  Quality: 59.00      Length: 59
  Ratio: 1.000      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-805-550-4 x BF655703 ..

Align seg 1/1 to: BF655703 from: 1 to: 315

1 MetLysLeuThrValLysThrLeuLysGlyThrHisPheGluIleArgVal 17
|||||
137 ATGAAGCTGACGGTGAAGACCTCAAGGGCAGCGACTTCGAGATCCGGGT 186
|||||
17  IGlProAsnAspThrIleMetAlaValLysLysAsnIleGluGluGlu 34
|||||
187 GCAGCCCAACGACACAGATTAAGCTGTCAAGAAAAACATCCAAGAGATAC 236
|||||
34  lngLysAspSerTyrProTrrpGlyGlnGlnLeuLeuIlePheAsnGly 50
|||||
237 AAGGAAAGGACAGCTATCCATGCGGGCAACAACGTGATTTCAATGGG 286
|||||
51  LysValLeuLysAspGluSerThrLeu 59
|||||
287 AAGGCTCTTGAAAGATGAAGATGACATG 313
|||||

seq_name: gb_est2:BE360535

seq_documentation_block:
LOCUS      BE360535      605 bp      mRNA      linear      EST 20-JUL-2000
DEFINITION D01_64_F06_b1_A002 Dark Grown 1 (D01) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION  BE360535
VERSION     BE360535.1 GI:9302092
KEYWORDS   EST.
SOURCE     Sorghum.
ORGANISM   Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 605)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
,L.H.

```

TITLE An EST database from Sorghum: dark-grown seedlings  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cordonnier-Pratt MM  
Department of Botany  
The University of Georgia  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 542 1805  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude polyA, vector and regions below phred quality 16. The threshold for highest quality sequence is 20.  
Seq primer: JEN REV  
High quality sequence stop: 567  
POLYA-No.

FEATURES  
source location/Qualifiers  
1..605  
/organism="Sorghum bicolor"  
/db\_xref="taxon:4558"  
/clone\_id="Dark grown 1 (DG1)"  
/note="Organ: 5-day-old dark-grown seedlings; Vector: lambda zap; Site\_1: XhoI; Site\_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 166 a 178 c 152 g 109 t

ORIGIN

alignment\_scores:  
Quality: 59.00 Length: 59  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-805-550-4 x BE360535 ..

Align seg 1/1 to: BE360535 from: 1 to: 605

1 MetTysLeuThrValLysThrLeuLysGlyThrHisPheGluIleArgVa 17  
|||||  
148 ATGAAGCTGACGCGTGAAGACCTCAAGGCGACACTTCGAGATCCGGGT 197  
|||||  
17 TGluproAsnAspThrIleMetAlaValLysAsnIleGluGluIleG 34  
|||||  
198 GCAGCCCAACGACACGATTATGGCTGTGAAGAAACATCGAAGATAC 247  
|||||  
34 TngLysAspSerTyrProTrpGlyGlnGlnLeuLeuIlePheAsnGly 50  
|||||  
248 AAGGAAAGACAGCTATTCATGCGGCAACACTGCTATTTCATATGG 297  
|||||  
51 LysValLeuLysAspGluSerThrLeu 59  
|||||  
298 AAGGCTTGAAGATGAAGATGATG 324

seq\_name: gb\_estl:AI612200

seq\_documentation\_block:  
LOCUS AI612200 374 bp mRNA linear EST 21-APR-1999  
DEFINITION 486083C02.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.  
ACCESSION AI612200  
VERSION AI612200.1 GI:4621367  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE  
AUTHORS Walbot,V.  
TITLE 1 (bases 1 to 374)  
JOURNAL Maize ESTs from various cDNA libraries sequenced at Stanford University  
COMMENT Unpublished (1999)

COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 486083 row: C column: 02.

FEATURES  
source location/Qualifiers  
1..374  
/organism="Zea mays"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone\_id="486 - leaf primordia cDNA library from Hake lab"  
/tissue\_type="leaf primordia"  
/dev\_stage="p7-p11 leaf"  
/lab\_host="E.coli XL1-Blue MFR"  
/note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA library."

BASE COUNT 96 a 93 c 59 g 126 t

ORIGIN

alignment\_scores:  
Quality: 58.00 Length: 58  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-805-550-4 x AI612200/rev ..

Align seg 1/1 to reverse of: AI612200 from: 1 to: 374

311 GUGLUASPGLUMETPROHISALAIIESERVALTHRPROGLUGLUGL 327  
|||||  
373 GAGGAGATGAATGCTCATGCTTACTGTACACCGAGAGACAGCA 324  
|||||  
327 UAlaIleGlyArgLeuGluSerMetGlyPheAspArgAlaArgValIleG 344  
|||||  
323 GGCATTGGACGCGCTTGACTCATGGCGGTTCACAGACAGACGCTTATG 274  
|||||  
344 LAlaPheLeuAlaCysAspArgAsnGluGluLeuAlaIleAsnTyrLeu 360  
|||||  
273 AAGCATTCCTTACCGCTGATGAGAACGAGACGACCTGAACAATCATCTC 224  
|||||  
361 LeuGluHisAlaGlyGluLysP 368  
|||||  
223 CTTGACATGCTGCTGAGGAGAT 200

seq\_name: gb\_estl:AW171897

seq\_documentation\_block:  
LOCUS AW171897 603 bp mRNA linear EST 12-NOV-1999  
DEFINITION 618053E05.x1 618 - Indred Tassel cDNA library Zea mays cDNA, mRNA sequence.  
ACCESSION AW171897  
VERSION AW171897.1 GI:6403422  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE  
AUTHORS Walbot,V.  
TITLE 1 (bases 1 to 603)  
JOURNAL Maize ESTs from various cDNA libraries sequenced at Stanford University  
COMMENT Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
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Tel: 650 723 2227  
Fax: 650 725 8221

Email: walbot@stanford.edu  
Plate: 618053 row: E column: 05.

FEATURES  
source Location/Qualifiers

1. 603

/organism="Zea mays"

/cultivar="Ohio43"

/db\_xref="taxon:4577"

/clone\_lib="618 - Inbred Tassel cDNA library"

/tissue\_type="tassel"

/dev\_stage="tassel length from 0.1 to 2.5 cm"

/lab\_host="XLOLR"

/note="Organ: tassel; Vector: PAD-GAL4-2.1 (Hybridap); Inbred tassel library from Schmidt lab"

BASE COUNT 173 a 114 c 149 g 167 t

ORIGIN

alignment\_scores:

Quality: 56.00 Length: 56

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-805-550-4 x AM171897 ..

Align seg 1/1 to: AM171897 from: 1 to: 603

313 AAGGLMETHFROHSAHALESERVALTHPROGLUINGLUALAI1 329

|||||

297 GATGAATGCTCAGCCATTAGTTACACACAGAGAGAGGCGCAT 346

|||||

329 EG1ATGLeuG1UsermetG1yPheasPARGALAARVAILleG1uA1AP 346

|||||

347 TGAACGGCTGATCCATGGGTTGACACAGACGCGTTATCGAACAT 396

|||||

346 heLeuAlaCysAspArgAsnGluGluLeuAlaAlaAsnTYrLeuGlu 362

|||||

397 TCTTACGCTCGATAGACAGACAGAGAGTACCAACTATCTCTTCTGAG 446

|||||

363 H1sAlaG1yG1uG1uAsp 368

|||||

447 CATGCTGTTGAGAGAGAT 464

seq\_name: gb\_est1:AA61449

seq\_documentation\_block:

LOCUS AA61449 220 bp mRNA linear EST 12-NOV-1997

DEFINITION ZEST00631 Maize leaf, Stratiagene #937005 Zea mays cDNA clone

csuh00631 5' end similar to RAD 23, mRNA sequence.

ACCESSION AA61449

VERSION AA61449.1 GI:2615440

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 220)

Baysdorfer, C.

The Maize CDNA Program

Unpublished (1993)

Contact: Baysdorfer C

California State University

Dept Biol Sci, California State Univ, Hayward, CA 94542

Tel: 5108834747

Fax: 5108834747

Email: cbaysdor@haywire.csu Hayward.edu

Seq primer: SK.

Location/Qualifiers

1..220

/organism="Zea mays"

/strain="B73"

/db\_xref="taxon:4577"

/clone="csuh00631"

/clone\_lib="Maize leaf, Stratiagene #937005"

/note="Vector: Uni-ZAP; Site\_1: EcoRI; Site\_2: XhoI; mRNA isolated from illuminated leaves and sheaths of 5 week old plant. cDNA directionally cloned into vector."

BASE COUNT 48 a 60 c 56 g 53 t

ORIGIN

alignment\_scores:

Quality: 41.00 Length: 41

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-805-550-4 x AA61449 ..

Align seg 1/1 to: AA61449 from: 1 to: 220

202 A1asAnThrThrAspArgAlaProThrg1yGluAlaG1yLeuSerG1yI1 218

|||||

94 GCAACACACACTGATCGAGCTCTACTGAGAGAGCTGCTCTGGAT 143

|||||

218 eProAsnThra1aProLeuAspLeuPheProG1yAlaSerAsnAlag 235

|||||

144 TCCAAACACCGCTCCACTAGATCTTTCCGACAGGCGCTTCCATGCTG 193

|||||

235 1yG1yG1yAlaG1yG1yPro 242

|||||

194 GAGGTGGTGGTGGTGGTGGACCA 216

seq\_name: gb\_est1:A1948181

seq\_documentation\_block:

LOCUS A1948181 460 bp mRNA linear EST 19-AUG-1999

DEFINITION 603037D08.x1 603 - stressed root cDNA library from Wang/Bohnert lab

Zea mays cDNA, mRNA sequence.

ACCESSION A1948181

VERSION A1948181.1 GI:5740491

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 460)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

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Email: walbot@stanford.edu

Plate: 603037 row: D column: 08.

Location/Qualifiers

1..460

/organism="Zea mays"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone\_lib="603 - stressed root cDNA library from Wang/Bohnert lab"

/tissue\_type="seedling"

/dev\_stage="salt stress"

/lab\_host="E. coli XL Gold"

/note="Organ: root; Vector: pBluescriptII SK(+); XR; Seedling stressed root cDNA library from Wang/Bohnert lab"

BASE COUNT 126 a 114 c 85 g 135 t

## ORIGIN

alignment\_scores:                   Quality:   39.00                   Length:   39  
                                       Ratio:   1.000                   Gaps:   0  
 Percent Similarity: 100.000       Percent Identity: 100.000

## alignment\_block:

US-09-805-550-4 x A1948181/rev ..

Align seg 1/1 to reverse of: A1948181 from: 1 to: 460

330 G1YAAGLEUGLUSERTCGLYPHEASPARGLAAGVAILLEGLUALAPH 346  
 331 GGACGCGCTTGAGTTCATGGGTTGCACAGACGCGCTTATGAAACATT 282  
 346 ELEUALACYSAPARGASNGLULEUALAALAAANTYRLLEUGLUNH 363  
 281 CTTACGCTCGCATAGGACGAGGAGCTACGACCAACTATCTCTTGAGC 232

363 ISALAGLYGLUGLUSAP 368  
 231 ATGCTGTGAGGAGAGAT 215

seq\_name: gb\_gss:BH255752

seq\_documentation\_block:

LOCUS BH255752 463 bp DNA linear GSS 29-NOV-2001  
 DEFINITION LDB5BAM0003D09f Zea mays L. DH51alpha methyl filtration maize leaf  
 genomic shotgun library Zea mays genomic clone LDB5BAM0003D09f, DNA  
 sequence.

ACCESSION BH255752  
 VERSION BH255752.1 GI:17150645  
 KEYWORDS GSS.

## SOURCE

ORGANISM Zea mays.  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 463)  
 Kim,S.W., Yu,Y., Lee,M.C., Yang,T.J., Main,D., Henry,D., Oates,R.  
 and Wing,R.A.

TITLE Genomic shotgun library from maize  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu  
 Seq primer: TAAATACGACTCCTACTATAGG  
 Class: shotgun

FEATURES  
 High quality sequence stop: 358.

## SOURCE

Location/Qualifiers  
 1. 463  
 /organism="Zea mays"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="LDB5BAM0003D09f"  
 /clone\_lib="Zea mays L. DH51alpha methyl filtration maize  
 leaf genomic shotgun library"  
 /tissue\_type="leaf"  
 /lab\_host="DH51alpha"  
 /note="Vector: pCUGIBLU-1; Site.1: Sau3A1; Site.2: Sau3A1;  
 methyl-filtration library, Nuclei DNA was digested with  
 Sau3A1, size fractionated and transformed to  
 E.coli DH51alpha."  
 BASE COUNT 109 a 92 c 90 g 168 t 4 others  
 ORIGIN

## alignment\_scores:

Quality:   37.00                   Length:   37  
                                       Ratio:   1.000                   Gaps:   0  
 Percent Similarity: 100.000       Percent Identity: 100.000

## alignment\_block:

US-09-805-550-4 x BH255752 ..

Align seg 1/1 to: BH255752 from: 1 to: 463

268 PROMETLEUVALGLUSEUERTSYSGINASPGLNILEUARGLEU 284  
 74 CCTATCTCTGCTTGAGTTCAGACAGACGAAATCCCAATTTCTAAGTTGAT 123  
 284 EUGLUANHNHASPGLUPHEUGLNULEUANAUGLUPROPHGLUG 301  
 124 TGGAGGAATCATGATGATTTCTTCACTTAATGAGCCCTTGAG 173  
 301 YGLYGLUGLY 304  
 174 GCGAGAGAGGG 184

seq\_name: gb\_est2:BE471046

seq\_documentation\_block:

LOCUS BE471046 409 bp mRNA linear EST 28-JUL-2000  
 DEFINITION WHE0283\_E11\_121S wheat drought-stressed seedling cDNA library  
 Triticum aestivum CDNA clone WHE0283\_E11\_121, mRNA sequence.

ACCESSION BE471046  
 VERSION BE471046.1 GI:9561525  
 KEYWORDS EST.

## SOURCE

ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 ; Triticeae; Triticum.  
 1 (bases 1 to 409)

TITLE  
 JOURNAL  
 COMMENT  
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han  
 ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,  
 Seaton,C.L. and Tong,J.C.  
 The structure and function of the expressed portion of the wheat  
 genomes - Drought-stressed seedling cDNA library  
 Unpublished (2000)

Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105959773  
 Fax: 510595818  
 Email: oanderson@nwp.usda.gov

Sequence have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20  
 Seq primer: Stragene SK primer.

FEATURES  
 Location/Qualifiers

1. 409  
 /organism="Triticum aestivum"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clone="WHE0283\_E11\_121"  
 /clone\_lib="Wheat drought-stressed seedling cDNA library"  
 /tissue\_type="Seedling without endosperm"  
 /dev\_stage="Five day old seedling"  
 /lab\_host="E. coli SOLR"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
 Site.1: EcoRI; Site.2: XhoI; Seeds were surface-sterilized  
 , germinated and grown aseptically in the dark at room  
 temperature on filter paper with water, nystatin and  
 cefotaxime in covered crystallization dishes. Five-day old  
 seedlings were incubated for one day at 90° RH. After  
 removing endosperm, seedlings were transferred to  
 desiccator jar containing saturated MgSO4 at room  
 temperature for 24 hr. The tissue, total RNA, and poly(A)  
 RNA were prepared, a cDNA library was made, and the cDNA

clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 119 a 94 c 125 g 71 t

ORIGIN

alignment\_scores:

Quality:	28.00	Length:	28
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment\_block:

US-09-805-550-4 x BE471046 ..

Align seg 1/1 to: BE471046 from: 1 to: 409

20 AsnAspThrIleMetAlaValLysAsnIleGluGlnIleGlnGly 36  
|||||  
226 AATGACACCATATGCTGCTCAGAGACATTCAGATTCAGAGAAA 275

36 SASPSerTyrProTyrGlnGlnLeuIle 47  
|||||  
276 GGATAGTATCATCGGCTCAACACATGCTGATT 309

seq\_name: gb\_est2:BE498178

seq\_documentation\_block:

LOCUS BE498178 432 bp mRNA linear EST 04-AUG-2000  
DEFINITION WHE0954\_E12\_J24ZS wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0954\_E12\_J24, mRNA sequence.

ACCESSION BE498178

VERSION BE498178.1 GI:9696795

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

REFERENCE 1 (bases 1 to 432)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library

Unpublished (2000)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1..432

source

the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 118 a 103 c 138 g 73 t

ORIGIN

alignment\_scores:

Quality:	28.00	Length:	28
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment\_block:

US-09-805-550-4 x BE498178 ..

Align seg 1/1 to: BE498178 from: 1 to: 432

20 AsnAspThrIleMetAlaValLysAsnIleGluGlnIleGlnGly 36  
|||||  
268 AATGACACCATATGCTGCTCAGAGACATTCAGATTCAGAGAAA 317

36 SASPSerTyrProTyrGlnGlnLeuIle 47  
|||||  
318 GGATAGTATCATCGGCTCAACACATGCTGATT 351

seq\_name: gb\_est2:BE517807

seq\_documentation\_block:

LOCUS BE517807 448 bp mRNA linear EST 08-AUG-2000  
DEFINITION WHE0803\_E10\_J19ZS wheat vernalized crown cDNA library Triticum aestivum cDNA clone WHE0803\_E10\_J19, mRNA sequence.

ACCESSION BE517807

VERSION BE517807.1 GI:9741837

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

REFERENCE 1 (bases 1 to 448)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

The structure and function of the expressed portion of the wheat genomes - Vernalized crown cDNA library

Unpublished (2000)

Contact: Olin Anderson

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800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1..448

source

phagemids in the TI Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 120 a 108 c 146 g 74 t

alignment\_scores:  
Quality: 28.00 Length: 28  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-805-550-4 x BE517807 ..

Align seg 1/1 to: BE517807 from: 1 to: 448

20 AsnAspThrIleMetAlaValLysAsnIleGlnGluIleGlnGly 36  
|||||  
286 AATGACACCATTTATGCTGTCAAGAACATTGAAGAGATTCAAGGAA 335

36 sAspSerTyrProTPrGlyGlnGlnLeuLeu 47  
|||||  
336 GGATAGTTATCCGTGGGCTCAACAACACTGCTGATT 369

seq\_name: gb\_est2:BE585808

seq\_documentation\_block:

LOCUS BE585808 725 bp mRNA linear EST 17-AUG-2000  
DEFINITION Est#2PT7\_E07\_051 KSU wheat Fusarium graminearum infected spike  
CDNA library Triticum aestivum CDNA clone Est#2PT7\_E07\_051, mRNA  
sequence.  
ACCESSION BE585808  
VERSION BE585808.1 GI:9838840  
KEYWORDS EST.  
SOURCE bread wheat.  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Triticum.  
1 (bases 1 to 725)  
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.  
The structure and function of the expressed portion of the wheat  
genomes - Kansas State University. Fusarium graminearum infected  
spike cDNA library  
Unpublished (2000)  
Contact: John Fellers  
US Department of Agriculture, Agriculture Research Service, Plant  
Science and Entomology Unit  
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State  
University, Manhattan, KS 66506, USA  
Tel: 785-532-2367  
Fax: 785-532-6167  
Email: jofell@alfalfa.ksu.edu

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
US Department of Agriculture, Agriculture Research Service, Plant  
Science and Entomology Unit  
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State  
University, Manhattan, KS 66506, USA  
Tel: 785-532-2367  
Fax: 785-532-6167  
Email: jofell@alfalfa.ksu.edu

Sequence have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20  
Seq primer: T7.  
Location/Qualifiers  
1..725

FEATURES  
Source  
/organism="Triticum aestivum"  
/cultivar="Suma13"  
/db\_xref="taxon:4565"  
/clone="Est#2PT7\_E07\_051"  
/clone\_lib="KSU wheat Fusarium graminearum infected spike  
cDNA library"  
/tissue\_type="Spoke"  
/dev\_stage="Adult plant"  
/lab\_host="E. coli JM109"  
/note="Vector: pGEM-T easy; Site:1: SacII; Site:2: SpeI;  
plants were grown in the greenhouse. Spikes were sprayed  
with Fusarium graminearum (at what stage). Total RNA, and  
poly(A) RNA were prepared from infected spikes. cDNA was

prepared using the SmartTM PCR cDNA synthesis kit from  
Clontech. cDNA was cloned into the pGEM-T easy vector  
from Promega."

BASE COUNT 197 a 196 c 203 g 128 t 1 others

alignment\_scores:  
Quality: 28.00 Length: 28  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-805-550-4 x BE585808 ..

Align seg 1/1 to: BE585808 from: 1 to: 725

20 AsnAspThrIleMetAlaValLysAsnIleGlnGluIleGlnGly 36  
|||||  
327 AATGACACCATTTATGCTGTCAAGAACATTGAAGAGATTCAAGGAA 376

36 sAspSerTyrProTPrGlyGlnGlnLeuLeu 47  
|||||  
377 GGATAGTTATCCGTGGGCTCAACAACACTGCTGATT 410

seq\_name: gb\_est2:BG629728

seq\_documentation\_block:

LOCUS BG629728 418 bp mRNA linear EST 19-APR-2001  
DEFINITION CC-eflicEL29M16a1 Tomato flower library from a mixture of  
developmental stages Lycopersicon esculentum CDNA clone  
CC-eflicEL29M16a1, mRNA sequence.  
ACCESSION BG629728  
VERSION BG629728.1 GI:13681214  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; eusteirids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 418)  
van der Hoeven,R.S. and Tanksley,S.D.  
ESTs from a tomato flower library  
Unpublished (2001)  
Contact: Rutgers S. van der Hoeven  
Cornell University  
252 Emerson Hall, Ithaca, NY 14850, USA  
Tel: 607 255 7886  
Fax: 607 255 6883  
Email: rv19@cornell.edu

3 prime sequence.  
Location/Qualifiers  
1..418

FEATURES  
Source  
/organism="Lycopersicon esculentum"  
/cultivar="E6203"  
/db\_xref="taxon:4081"  
/clone="CC-eflicEL29M16a1"  
/clone\_lib="tomato flower library from a mixture of  
developmental stages"  
/tissue\_type="developing flower buds and open flowers"  
/dev\_stage="4-8 week old plants"  
/lab\_host="XL0LR"  
/note="Vector: pBK CMV; Site:1: EcoRI; Site:2: XhoI;  
flowers and flower buds were collected from greenhouse  
grown plants and used for library construction (cLEL). "

BASE COUNT 126 a 101 c 58 g 133 t

alignment\_scores:  
Quality: 24.00 Length: 24  
Ratio: 1.000 Gaps: 0



Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-805-550-4 x BG629728/rev ..

Align seg 1/1 to reverse of: BG629728 from: 1 to: 418

```
342 ValIleGIuAlaPheLeuAlaCysAspArgAsnGIuGIuLeuAlaAlaAs 358
|||||
238 GTCATTTGAAGCTTTTGTGCTGTGATCGCAATGAGAACTGGCTGCCAA 189
|||||
358 nTyrLeuEnGIuHisAlaGIy 365
|||||
188 TTATCTGTGGAGCATGCAGGA 167
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